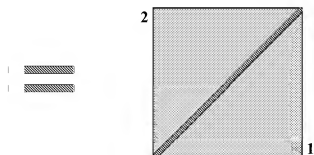


Sequence 1: SEQ ID NO:1

Length = 1783 (1 .. 1783)

Sequence 2: gi|184371|Human hepsin mRNA, complete cds (GenBank entry M18930)

Length = 1783 (1 .. 1783)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 3428 bits (1783), Expect = 0.0
Identities = 1783/1783 (100%), Gaps = 0/1783 (0%)
Strand=Plus/Plus

Query	1	TCGAGCCCGCTTTCCAGGGACCCCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGC	60
Sbjct	1	TCGAGCCCGCTTTCCAGGGACCCCTACCTGAGGGCCACAGGTGAGGCAGCCTGGCCTAGC	60
Query	61	AGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCC	120
Sbjct	61	AGGCCCCACGCCACCGCCTCTGCCTCCAGGCCGCCCGCTGCTGCGGGGCCACCATGCTCC	120
Query	121	TGCCCCAGGCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGC	180
Sbjct	121	TGCCCCAGGCCTGGAGACTGACCCGACCCCGGCACTACCTCGAGGCTCCGCCCCACCTGC	180
Query	181	TGGACCCAGGGTCCCAACCTGGCCAGGAGGTGAGCCAGGGAATCATTAAACAAGAGGCA	240
Sbjct	181	TGGACCCAGGGTCCCAACCTGGCCAGGAGGTGAGCCAGGGAATCATTAAACAAGAGGCA	240
Query	241	GTGACATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGG	300
Sbjct	241	GTGACATGGCGCAGAAGGAGGGTGGCCGGACTGTGCCATGCTGCTCCAGACCCAAGGTGG	300
Query	301	CAGTCTCTACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCCA	360
Sbjct	301	CAGTCTCTACTGCGGGGACCTGCTACTTCTGACAGCCATCGGGGCGGCATCTGGGCCA	360

Query	361	TTGTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCAGCTCTG	420
Sbjct	361	TTGTGGCTGTTCTCCTCAGGAGTGACCAGGAGCCGCTGTACCCAGTGCAGGTCAGCTCTG	420
Query	421	CGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCT	480
Sbjct	421	CGGACGCTCGGCTCATGGTCTTTGACAAGACGGAAGGGACGTGGCGGCTGCTGTGCTCCT	480
Query	481	CGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCAC	540
Sbjct	481	CGCGCTCCAACGCCAGGGTAGCCGGACTCAGCTGCGAGGAGATGGGCTTCTCAGGGCAC	540
Query	541	TGACCCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCACGTGCGGCTTCTTCT	600
Sbjct	541	TGACCCACTCCGAGCTGGACGTGCGAACGCGGGCGCCAATGGCACGTGCGGCTTCTTCT	600
Query	601	GTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTG	660
Sbjct	601	GTGTGGACGAGGGGAGGCTGCCCCACACCCAGAGGCTGCTGGAGGTATCTCCGTGTGTG	660
Query	661	ATTGCCCCAGAGGCGTTCCTTGGCGGCCATCTGCCAAGACTGTGGCCGCGAGGAAGCTGC	720
Sbjct	661	ATTGCCCCAGAGGCGTTCCTTGGCGGCCATCTGCCAAGACTGTGGCCGCGAGGAAGCTGC	720
Query	721	CCGTGGACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCA	780
Sbjct	721	CCGTGGACCGCATCGTGGGAGGCCGGGACACAGCTTGGGCCGCTGGCCGTGGCAAGTCA	780
Query	781	GCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGC	840
Sbjct	781	GCCTTCGCTATGATGGAGCACACCTCTGTGGGGGATCCCTGCTCTCCGGGACTGGGTGC	840
Query	841	TGACAGCCGCCCACTGCTTCCCGAGCGGAACCGGGTCTGTGCCGATGGCGAGTGTTTG	900
Sbjct	841	TGACAGCCGCCCACTGCTTCCCGAGCGGAACCGGGTCTGTGCCGATGGCGAGTGTTTG	900
Query	901	CCGGTGCCGTGGCCCAAGCCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCT	960
Sbjct	901	CCGGTGCCGTGGCCCAAGCCCTCTCCCCACGGTCTGCAGCTGGGGGTGCAGGCTGTGGTCT	960
Query	961	ACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTG	1020
Sbjct	961	ACCACGGGGGCTATCTTCCCTTTCGGGACCCCAACAGCGAGGAGAAACAGCAACGATATTG	1020
Query	1021	CCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCCTCC	1080
Sbjct	1021	CCCTGGTCCACCTCTCCAGTCCCCTGCCCTCACAGAATACATCCAGCCTGTGTGCCCTCC	1080
Query	1081	CAGTGC CGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACA	1140
Sbjct	1081	CAGTGC CGGCCAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACA	1140
Query	1141	CGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCA	1200
Sbjct	1141	CGCAGTACTATGGCCAAACAGGCCGGGGTACTCCAGGAGGCTCGAGTCCCATAATCAGCA	1200

Query	1201	ATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTG	1260
Sbjct	1201	ATGATGTCTGCAATGGCGCTGACTTCTATGGAAACCAGATCAAGCCCAAGATGTTCTGTG	1260
Query	1261	CTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGCGCACAGCGGTGGTCCCTTTGTGT	1320
Sbjct	1261	CTGGCTACCCCGAGGGTGGCATTGATGCCTGCCAGGCGCACAGCGGTGGTCCCTTTGTGT	1320
Query	1321	GTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCA	1380
Sbjct	1321	GTGAGGACAGCATCTCTCGGACGCCACGTTGGCGGCTGTGTGGCATTGTGAGTTGGGGCA	1380
Query	1381	CTGGCTGTGCCCTGGGCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGT	1440
Sbjct	1381	CTGGCTGTGCCCTGGGCCAGAAAGCCAGGCGTCTACACCAAAGTCAGTGACTTCCGGGAGT	1440
Query	1441	GGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGAC	1500
Sbjct	1441	GGATCTTCCAGGCCATAAAGACTCACTCCGAAGCCAGCGGCATGGTGACCCAGCTCTGAC	1500
Query	1501	CGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACG	1560
Sbjct	1501	CGGTGGCTTCTCGCTGCGCAGCCTCCAGGGCCCGAGGTGATCCCGGTGGTGGGATCCACG	1560
Query	1561	CTGGGCCGAGGATGGGACGTTTTTCTTCTTTGGGCCCAGGTCCACAGGTCCAAGGACACCCCT	1620
Sbjct	1561	CTGGGCCGAGGATGGGACGTTTTTCTTCTTTGGGCCCAGGTCCACAGGTCCAAGGACACCCCT	1620
Query	1621	CCCTCCAGGGTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCACT	1680
Sbjct	1621	CCCTCCAGGGTCCTCTCTTCCACAGTGGCGGGCCCACTCAGCCCCGAGACCAACCACT	1680
Query	1681	CACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCC	1740
Sbjct	1681	CACCTCCTGACCCCATGTAAATATTGTTCTGCTGTCTGGGACTCCTGTCTAGGTGCCC	1740
Query	1741	CTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT	1783
Sbjct	1741	CTGATGATGGGATGCTCTTTAAATAATAAAGATGGTTTTGATT	1783